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1: Gene. 1994 May 27;143(1):79-83.

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## The penicillin amidase of *Arthrobacter viscosus* (ATCC 15294).

Konstantinović M, Marjanović N, Ljubijankić G, Glisin V.

Institute of Molecular Genetics and Genetic Engineering, Belgrade, Yugoslavia.

The nucleotide (nt) sequence of the gene encoding penicillin G amidase (PA) of *Arthrobacter viscosus* strain ATCC 15,294 was determined. The sequence contained an open reading frame of 2406 nt with a G+C content of 37%. The deduced amino-acid sequence shows significant homology with other so far identified beta-lactam amidases of Gram- bacteria.

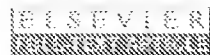
Publication Types:

- Comparative Study
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PMID: 8200542 [PubMed - indexed for MEDLINE]

2: Arch Biochem Biophys. 1997 Feb 1;338(1):22-8.

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## Cloning, sequencing, and expression of *Arthrobacter protophormiae* endo-beta-N-acetylglucosaminidase in *Escherichia coli*.

Takegawa K, Yamabe K, Fujita K, Tabuchi M, Mita M, Izu H, Watanabe A, Asada Y, Sano M, Kondo A, Kato I, Iwahara S.

Department of Bioresource Science, Faculty of Agriculture, Kagawa University, Miki-cho, Japan. [takegawa@ag.kagawa-u.ac.jp](mailto:takegawa@ag.kagawa-u.ac.jp)

The gene encoding endo-beta-N-acetylglucosaminidase from *Arthrobacter protophormiae* (Endo-A) was cloned, and its nucleotide sequence was determined. A single open reading frame consisting of 1935 base pairs and encoding a polypeptide composed of signal peptides of 24 amino acids and a mature protein of 621 amino acids was found. The primary structure of Endo-A exhibited significant homology with FO1F.10 gene product from *Caenorhabditis elegans* and weak homology with peptide-N4-(N-acetyl-beta-D-glucosaminy)asparagine amidase from *Flavobacterium meningosepticum* and chitinase from *Streptomyces olivaceoviridis*. However, the enzyme had no significant homology with any previously reported endo-beta-N-acetylglucosaminidases. Transformed *Escherichia coli* cells carrying the 4.5-kb fragment expressed Endo-A activity. This enzyme activity was detected in the medium as well as in the periplasmic space of cells under the control of the Endo-A gene promoter. The recombinant Endo-A was efficiently isolated from the periplasmic space of the cells. N-terminal sequence analysis revealed that native and recombinant Endo-A have the same N-terminus. Recombinant and native Endo-A also showed very similar optimum pH profiles and transglycosylation activity.

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